

**INFORMATION  
DISCLOSURE  
STATEMENT**

Atty. Docket No.: 265.00400101	Serial No.: 10/817,530
Applicant(s): Braun et al.	Confirmation No.: 4868
Application Filing Date: April 2, 2004	Group: 1631
Information Disclosure Statement mailed:	April 18, 2005

**U.S. PATENT DOCUMENTS**

Examiner Initial	Copy Enclosed	Document Number	Date	Name	Class	Subclass	Filing Date If Appropriate
LC		5,845,049	12/01/98	Wu			
LC		5,878,373	03/02/99	Cohen et al.			
LC		6,512,981	01/28/03	Eisenberg et al.			

**FOREIGN PATENT DOCUMENTS**

Examiner Initial	Copy Enclosed	Document Number	Date	Country	Class	Subclass	Translation	
							Yes	No
		None						

**OTHER DOCUMENTS (Including Authors, Title, Date, Pertinent Papers, etc.)**

Examiner Initial	Copy Enclosed	Document Description
LC	X	Altschul et al., "Grapped BLAST and PSI-BLAST: a new generation of protein database search programs," <i>Nucleic Acids Res</i> , 1997;25(17):3389-3402.
LC	X	Bairoch et al., "The SWISS-PROT protein sequence database and its supplement TrEMBL in 2000," <i>Nucleic Acids Res</i> , 2000;28(1):45-48.
LC	X	Ben-Hur et al., "Remote homology detection: a motif based approach," <i>Bioinformatics</i> , 2003;19(Suppl. 1):i26-i33.
LC	X	Benner et al., "Amino acid substitution during functionally constrained divergent evolution of protein sequences," <i>Protein Eng.</i> , 1994;7:1323-1332.
S	X	"BLAST." [online]. NCBI Blast. National Institute of Health. [retrieved on 2004-07-06]. Retrieved from the Internet:<http://www.ncbi.nlm.nih.gov/BLAST/>;1 pg.
LC	X	Bowie et al., "A method to identify protein sequences that fold into a known three-dimensional structure," <i>Science</i> , 1991;253:164-170.
LC	X	Brenner et al., "The ASTRAL compendium for protein structure and sequence analysis," <i>Nucleic Acids Res.</i> , 2000;28:254-256.
LC	X	Chandonia et al., "ASTRAL compendium enhancements," <i>Nucleic Acids Res.</i> , 2002;30(1):260-263.
LC	X	Chothia et al., "The relation between the divergence of sequence and structure in proteins," <i>EMBO J</i> , 1986;5: 823-826.

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/Lori Clow/

**Date Considered**

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10	X	"ClustalW." [online]. European Bioinformatics Institute (EMBL-EBI) [retrieved on 2004-07-06]. Retrieved from the Internet: < <a href="http://www.ebi.ac.uk/clustalw/">http://www.ebi.ac.uk/clustalw/</a> >; 2 pgs.
LC	X	Dubchak et al., "Recognition of a protein fold in the context of the SCOP classification," <i>Proteins</i> , 1999;35:401-407.
LC	X	Eddy, S.R., "Profile hidden Markov models," <i>Bioinformatics</i> , 1998;14:755-763.
13	X	"Emotif Maker." [online]. Biochemistry. Standford University, Standford, CA [retrieved on 2004-07-06]. Retrieved from the Internet: < <a href="http://fold.stanford.edu/emotif/emotif-maker.html">http://fold.stanford.edu/emotif/emotif-maker.html</a> >; 2 pgs.
LC	X	Falquet et al., "The PROSITE database, its status in 2002," <i>Nucleic Acids Res</i> , 2002;30: 235-238.
LC	X	Gough et al., "SUPERFAMILY: HMMs representing all proteins of known structure. SCOP sequence searches, alignments and genome assignments," <i>Nucleic Acids Res</i> , 2002;30: 268-272.
LC	X	Gribskov et al., "Identification of sequence patterns with profile analysis," <i>Methods Enzymol</i> , 1996;266:198-212.
LC	X	Henikoff et al., "Increased coverage of protein families with the Blocks Database servers," <i>Nucleic Acids Res</i> , 2000;28:228-230.
LC	X	Henikoff et al., "Blocks+: a non-redundant database of protein alignment blocks derived from multiple compilations," <i>Bioinformatics</i> , 1999, 15:471-479.
LC	X	Henikoff et al., "Protein family classification based on searching a database of blocks," <i>Genomics</i> , 1994;19:97-107.
LC	X	Higgins et al., "Multiple sequence alignment," <i>Methods Mol Biol.</i> , 2000;143: 1-18.
LC	X	Holm et al., "Mapping the protein universe," <i>Science</i> , 2000;273:595-602.
LC	X	Kelley et al., "Enhanced genome annotation using structural profiles in the program 3D-PSSM," <i>J Mol Biol</i> , 2000;299: 499-520.
LC	X	Kostich et al., "Human members of the eukaryotic protein kinase family," <i>Genome Biol</i> , 2002;3:43.
LC	X	Kullback et al., "On information sufficiency," <i>Ann Math Stat</i> , 1951;22: 79-86.
LC	X	Lo Conte et al., "SCOP database in 2002: refinements accommodates structural genomics," <i>Nucleic Acids Res</i> , 2002;30: 264-267.

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LC	X	Marcotte et al., "A combined algorithm for genome-wide prediction of protein function," <i>Nature</i> , 1999;402:83-86.
LC	X	Marcotte, E.M., "Computational genetics: finding protein function by nonhomology methods," <i>Curr Opin. Struct. Biol.</i> , 2000;10:359-365.
LC	X	Martelli et al., "A sequence-profile-based HMM for predicting and discriminating beta barrel membrane proteins," <i>Bioinformatics</i> , 2002;18: S46-53.
LC	X	Mathura et al., "Identifying Property Based Sequence Motifs in Protein Families and Superfamilies: Application to DNase I related endonucleases," <i>Bioinformatics</i> , 2003;19(11):1381-1390.
LC	X	Mathura et al., "Automated Generation of Property Based Motifs to Search for Functional Neighbors and to Improve Sequence Alignments," <i>5th Meeting on the Critical Assessment of Techniques for Protein Structure Prediction, CASP5</i> , Asilomar Conference Center, Pacific Grove, CA, December 1-5, 2002: A-178-179.
LC	X	Mathura et al., "Identifying Property Based Sequence Motifs in Protein Families and Superfamilies: Application to APE," <i>2002 Bioinformatics Symposium</i> , Rice University, Houston, TX, October 14-15, 2002: 37.
LC	X	Mathura et al., "Defining Physical-chemical Properties based motifs specific for members of the APE family of DNA repair proteins," <i>7th Structural Biology Symposium</i> , UTMB, Galveston, TX, May 17-19, 2002:93.
LC	X	Mathura et al., "Sequence and Structural Analysis of APE 1 Protein Family Using Physical-chemical Properties Based Motifs," <i>RECOMB, Currents in Computational Molecular Biology 2002</i> , Washington, DC.: 191-192.
LC	X	Mathura et al., "Physical-chemical properties based motifs for annotating protein sequences from genomic data," <i>Molecular Genomics 2002: Profiling of Gene Expression</i> , UTMB, Galveston, TX, April 5-7, 2002:35.
LC	X	Mathura et al., "Quantitative Descriptors for Amino Acids Based on Physico-Chemical Properties using Vector Representation," <i>Keck 2000 Symposium</i> , Baylor College of Medicine and Rice University, Houston, TX, October 16-17, 2000: 33.
LC	X	Mathura et al., "A New Vector Representation of Amino Acids Based on Large Number of Physico-Chemical Properties," <i>Fifth Annual Structural Biology Symposium</i> , UTMB, Galveston, TX, May 19-21, 2000: 54.
LC	X	Mehta et al., "Recognizing very distant sequence relationships among proteins by family profile analysis," <i>Proteins</i> , 1999;35:387-400.

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LC	X	Nagano et al., "One fold with many functions: the evolutionary relationships between TIM barrel families based on their sequences, structures and functions," <i>J Mol Biol</i> , 2002;321:741-765.
LC	X	Norin et al., "Structural proteomics: developments in structure-to-function predictions," <i>Trends Biotechnol.</i> , 2002;20:79-84.
LC	X	Overbeek et al., "The use of gene clusters to infer functional coupling," <i>Proc Natl Acad Sci USA</i> , 16 March 1999;96(6):2896-2901.
LC	X	Oezguen et al., "APE1: Identifying Motifs by MASIA and Metalion Position by MD-Simulations," <i>Keck Center 2001 Annual Research Conference</i> , Galveston, TX, September 21, 2001:35.
LC	X	Press et al., "Numerical Recipes in C: The Art of Scientific Computing," 1999, Cambridge University Press, New York.
43	X	"Prosite Database of protein families and domains." [online]. Exasy Prosite.[retrieved on 2004-07-06]. Retrieved from the Internet: < <a href="http://us.expasy.org/prosite/">http://us.expasy.org/prosite/</a> >;2 pgs.
LC	X	Rigoutsos et al., "Dictionary-driven protein annotation," <i>Nucleic Acids Res</i> , 2002;30:3901-3916.
LC	X	Rison et al., "Comparison of functional annotation schemes for genomes," <i>Funct Integr. Genomics</i> , 2000;1:56-69.
LC	X	Rychlewski et al., "Comparison of sequence profiles. Strategies for structural predictions using sequence information," <i>Protein Sci</i> , 2000;9:232-241.
LC	X	Schaffer et al., "IMPALA: matching a protein sequence against a collection of PSI-BLAST-constructed position-specific score matrices," <i>Bioinformatics</i> , 1999;16:1000-1011.
LC	X	Schaffer et al., "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements," <i>Nucleic Acids Res</i> , 2001;29:2994-3005.
LC	X	Schein et al., "Total sequence decomposition distinguishes functional modules, "molegos" in apurinic/apyrimidinic endonucleases," <i>BMC Bioinformatics</i> , 2002;3:37.
LC	X	Schein et al., "Structural and Functional Motifs of Apurinic/Apyrimidinic Endonuclease," <i>Sealy Center for Molecular Science, Science Forum</i> , UTMB, Galveston, TX, March 20, 2002: 7.

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LC	X	Schein et al., "Structural and Functional Motifs of Apurinic/Apyrimidinic Endonuclease," <i>Keystone Symposia Structural Genomics: From Gene Sequence to Function</i> , Breckenridge, CO, January 5-11, 2002:
LC	X	Schein et al., "Defining the mode of action of APE1 using MASIA motif searching, MD-simulations and site directed mutagenesis," <i>6th Annual Structural Biology Symposium</i> , UTMB Galveston, TX, May 18-20, 2001: 83.
LC	X	Truong et al., "Identification and characterization of subfamily-specific signature in a large protein superfamily by a hidden Markov model approach," <i>BMC Bioinformatics</i> , 2002;3(1).
LC	X	Unushihara, H., "Functional genomics of the social amoebae, Dictyostelium discoideum," <i>Mol. Cell</i> , 2002;13:1-4.
LC	X	Venkatarajan et al., "New quantitative descriptors of amino acids based on multidimensional scaling of a large number of physical -chemical properties," <i>J Mol Model</i> , 2001;7:445-453.
LC	X	Waterston et al., "On the sequencing of the human genome," <i>Proc. Natl. Acad. Sci USA</i> , 2002;99(6):3712-3716.
LC	X	Yona et al., "Within the twilight zone: a sensitive profile-profile comparison tool based on information theory," <i>J Mol Biol.</i> , 2002;315: 1257-1275.
LC	X	Zhu et al., "MASIA: recognition of common patterns and properties in multiple aligned protein sequences," <i>Bioinformatics</i> , 2000;16:950-951.

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